Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:25:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013280.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013280.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:25:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013280.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,546,117
Mapped reads	1,252,054 / 80.98%
Unmapped reads	294,063 / 19.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,933 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	175,169 / 11.33%
Duplication rate	11.06%
Clipped reads	742,422 / 48.02%

2.2. ACGT Content

Number/percentage of A's	21,658,974 / 27.24%
Number/percentage of C's	14,389,253 / 18.1%
Number/percentage of T's	25,575,039 / 32.17%
Number/percentage of G's	17,869,702 / 22.47%
Number/percentage of N's	18,842 / 0.02%
GC Percentage	40.57%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.3212

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

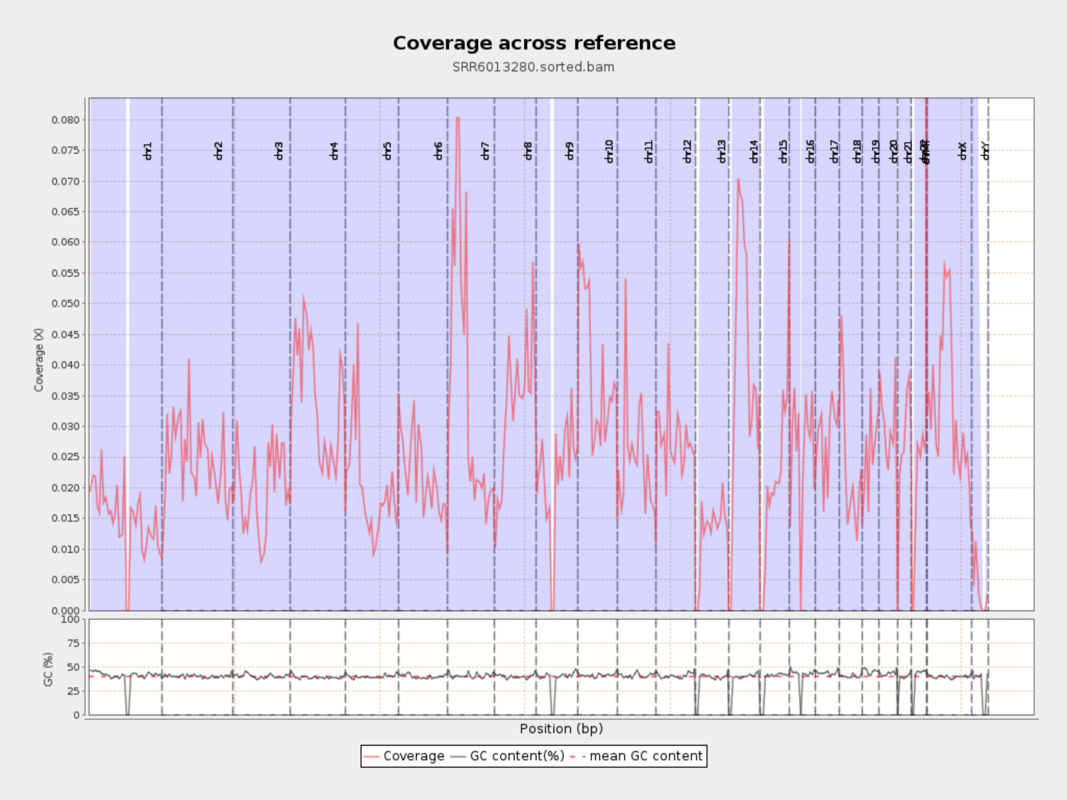
General error rate	0.95%
Mismatches	744,334
Insertions	5,786
Mapped reads with at least one insertion	0.46%
Deletions	30,060
Mapped reads with at least one deletion	2.37%
Homopolymer indels	43.56%

2.6. Chromosome stats

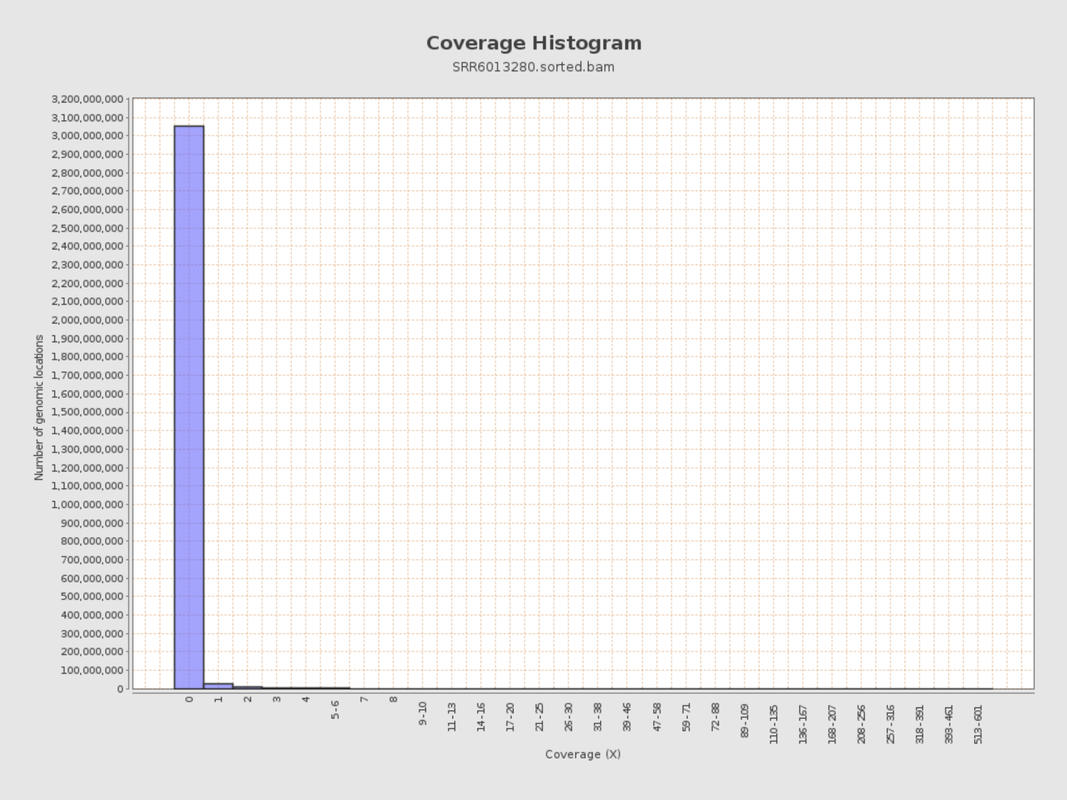
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3703850	0.0149	0.3322
chr2	243199373	5986683	0.0246	0.372
chr3	198022430	3936665	0.0199	0.2238
chr4	191154276	6681372	0.035	0.3051
chr5	180915260	3660616	0.0202	0.2255
chr6	171115067	3812445	0.0223	0.2623
chr7	159138663	5801495	0.0365	0.55

chr8	146364022	4877684	0.0333	0.4443
chr9	141213431	3082606	0.0218	0.2823
chr10	135534747	5387109	0.0397	0.3722
chr11	135006516	3333225	0.0247	0.2819
chr12	133851895	3733299	0.0279	0.267
chr13	115169878	1453911	0.0126	0.1795
chr14	107349540	4313678	0.0402	0.3301
chr15	102531392	2107722	0.0206	0.2256
chr16	90354753	2354825	0.0261	0.2622
chr17	81195210	2289394	0.0282	0.2837
chr18	78077248	1834397	0.0235	0.4627
chr19	59128983	1527545	0.0258	0.3072
chr20	63025520	1908292	0.0303	0.2862
chr21	48129895	1285559	0.0267	0.2619
chr22	51304566	984436	0.0192	0.219
chrMT	16571	33267	2.0075	2.6283
chrX	155270560	5247228	0.0338	0.3059
chrY	59373566	226133	0.0038	0.1067

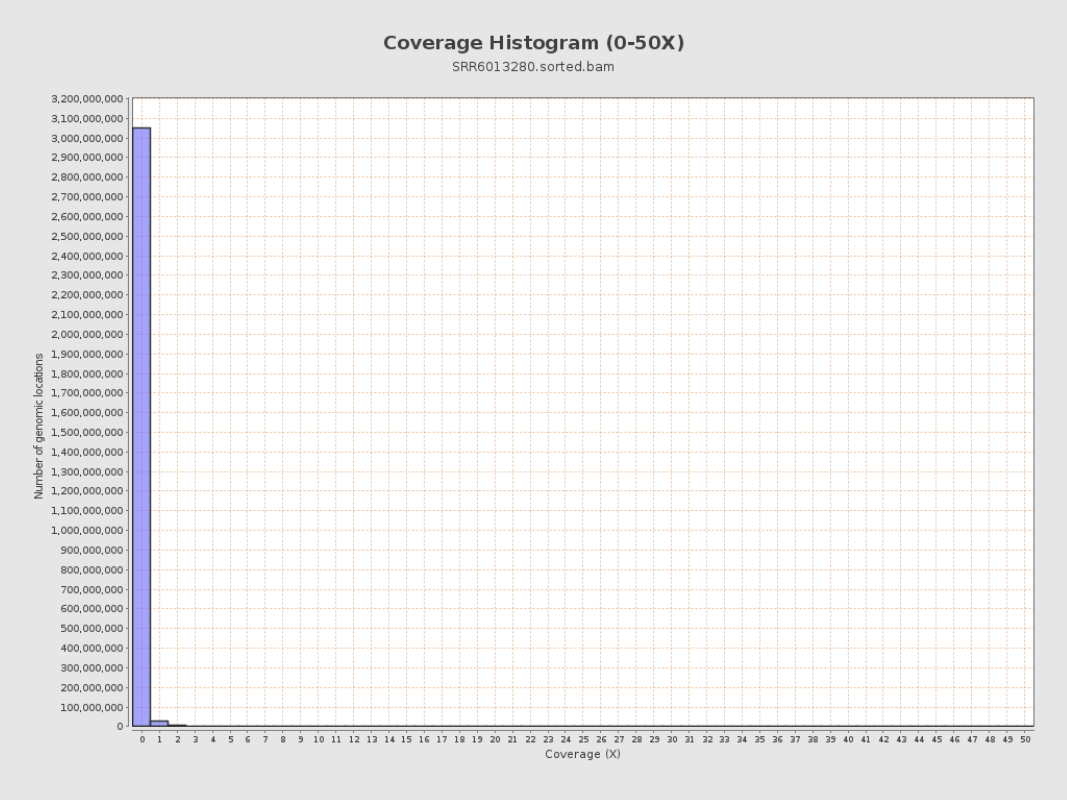
3. Results : Coverage across reference



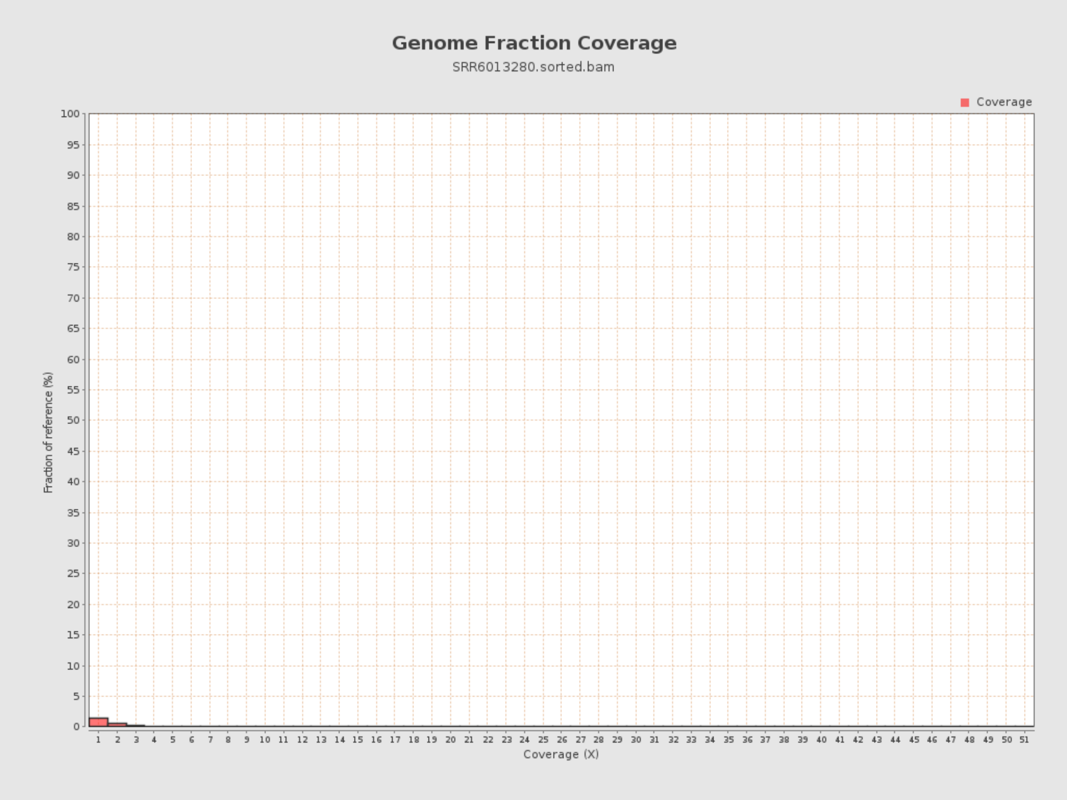
4. Results : Coverage Histogram



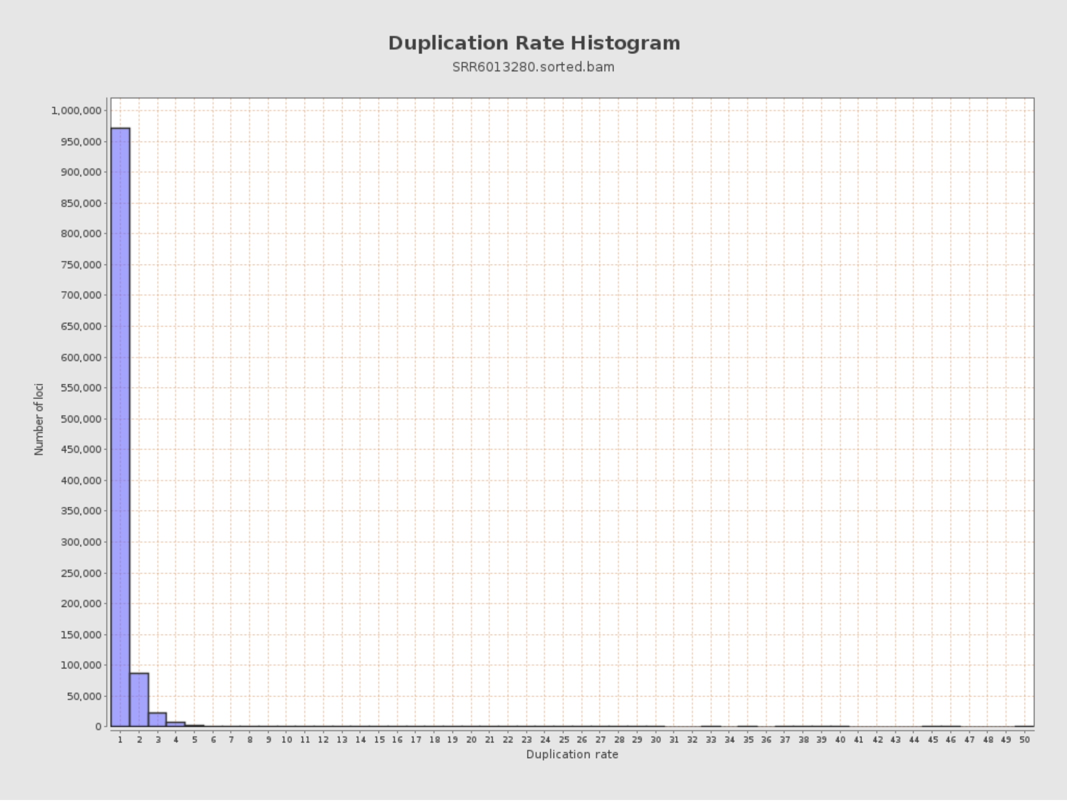
5. Results : Coverage Histogram (0-50X)



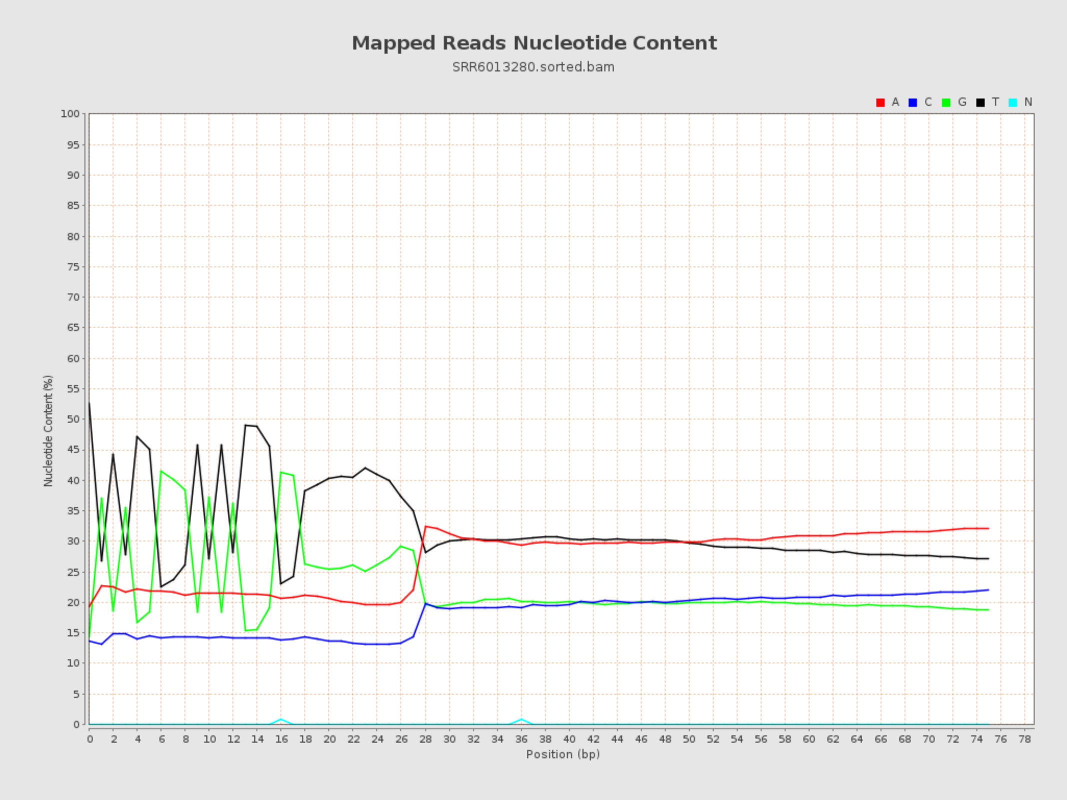
6. Results : Genome Fraction Coverage



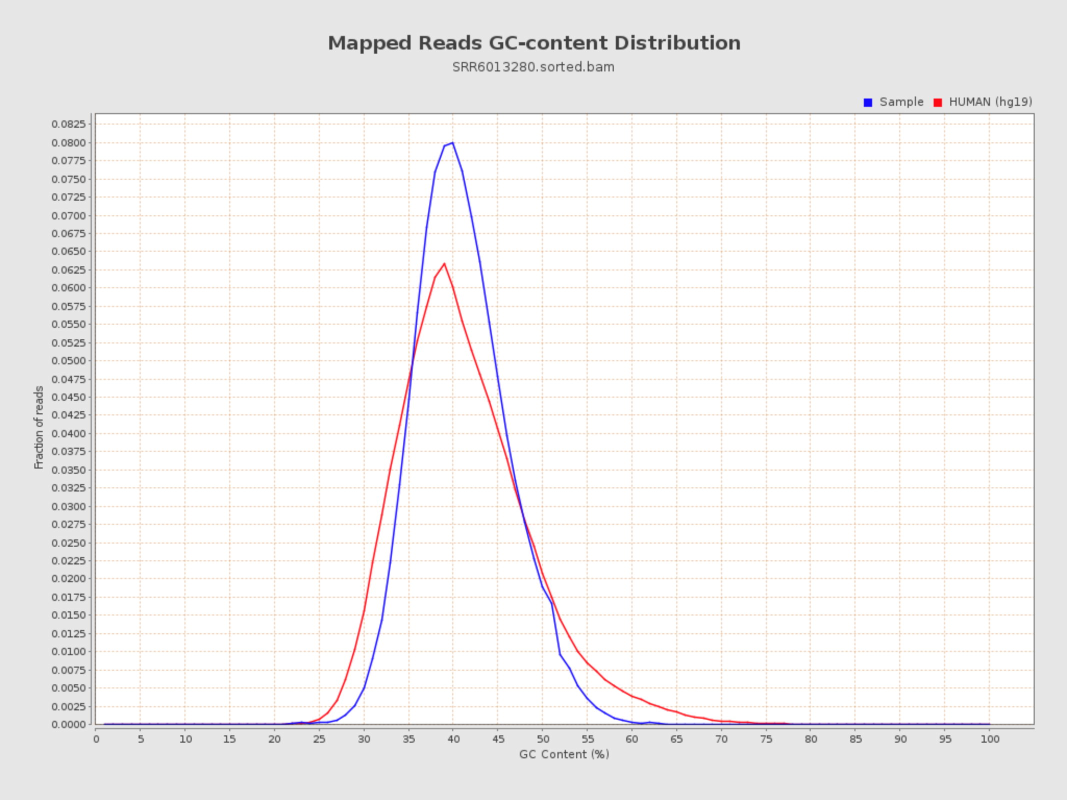
7. Results : Duplication Rate Histogram



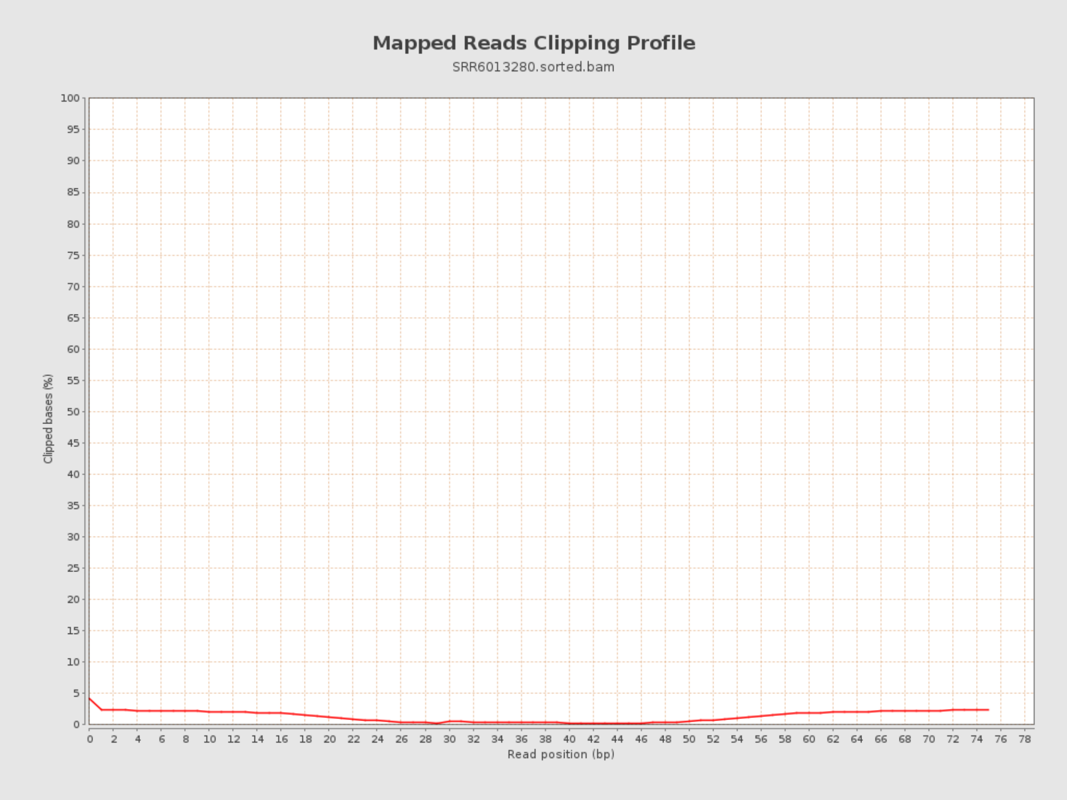
8. Results : Mapped Reads Nucleotide Content



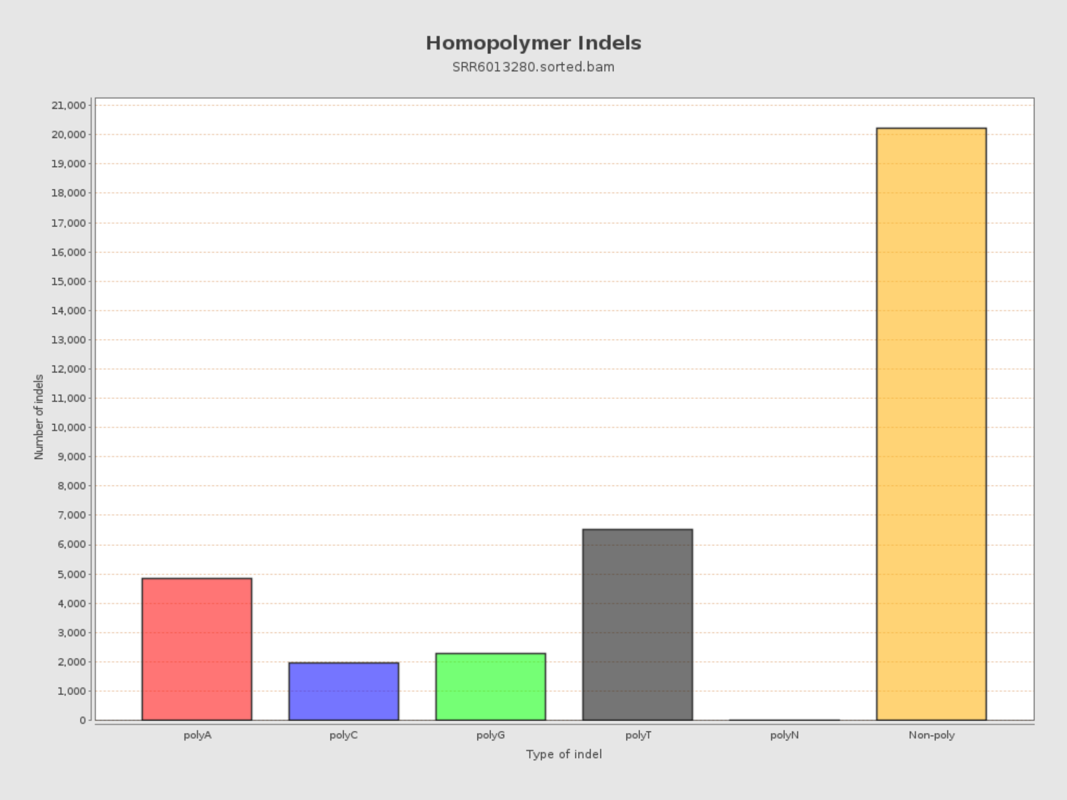
9. Results : Mapped Reads GC-content Distribution



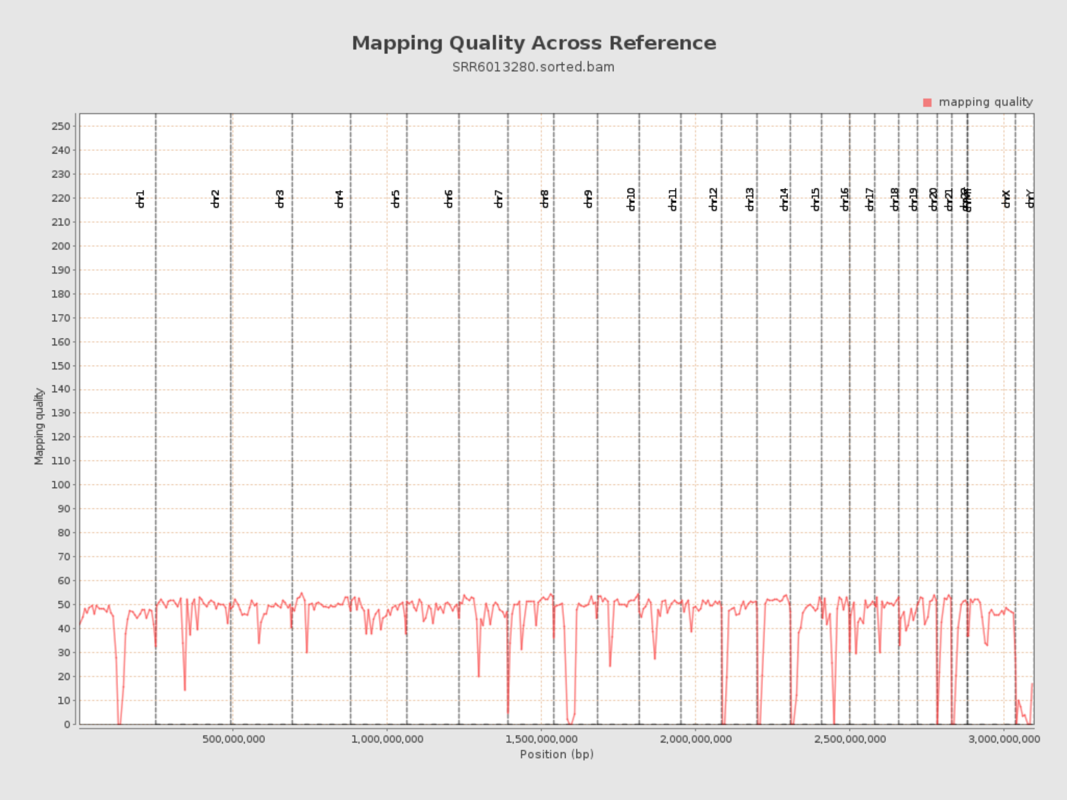
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram